

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: POTTER, ANDREW A.
REDMOND, MARK J.
HUGHES, HUW P.A.

(ii) TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN CHIMERAS

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: REED & ROBINS
(B) STREET: 285 HAMILTON AVENUE, SUITE 200
(C) CITY: PALO ALTO
(D) STATE: CALIFORNIA
(E) COUNTRY: UNITED STATES OF AMERICA
(F) ZIP: 94301

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/455,970
(B) FILING DATE: 31-MAY-1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/960,932
(B) FILING DATE: 14-OCT-1992

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: ROBINS, ROBERTA L.
(B) REGISTRATION NUMBER: 33,208
(C) REFERENCE/DOCKET NUMBER: 9001-0016.10

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 327-3400
(B) TELEFAX: (415) 327-3231

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2794 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..2778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCT ACT GTT ATA GAT CTA AGC TTC CCA AAA ACT GGG GCA AAA AAA Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys	48
1 5 10 15	
ATT ATC CTC TAT ATT CCC CAA AAT TAC CAA TAT GAT ACT GAA CAA GGT Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly	96
20 25 30	
AAT GGT TTA CAG GAT TTA GTC AAA GCG GCC GAA GAG TTG GGG ATT GAG Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu	144
35 40 45	
GTA CAA AGA GAA GAA CGC AAT AAT ATT GCA ACA GCT CAA ACC AGT TTA Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu	192
50 55 60	
GGC ACG ATT CAA ACC GCT ATT GGC TTA ACT GAG CGT GGC ATT GTG TTA Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu	240
65 70 75 80	
TCC GCT CCA CAA ATT GAT AAA TTG CTA CAG AAA ACT AAA GCA GGC CAA Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln	288
85 90 95	
GCA TTA GGT TCT GCC GAA AGC ATT GTA CAA AAT GCA AAT AAA GCC AAA Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys	336
100 105 110	
ACT GTA TTA TCT GGC ATT CAA TCT ATT TTA GGC TCA GTA TTG GCT GGA Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly	384
115 120 125	
ATG GAT TTA GAT GAG GCC TTA CAG AAT AAC AGC AAC CAA CAT GCT CTT Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu	432
130 135 140	
GCT AAA GCT GGC TTG GAG CTA ACA AAT TCA TTA ATT GAA AAT ATT GCT Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala	480
145 150 155 160	
AAT TCA GTA AAA ACA CTT GAC GAA TTT GGT GAG CAA ATT AGT CAA TTT Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe	528
165 170 175	
GGT TCA AAA CTA CAA AAT ATC AAA GGC TTA GGG ACT TTA GGA GAC AAA Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys	576
180 185 190	
CTC AAA AAT ATC GGT GGA CTT GAT AAA GCT GGC CTT GGT TTA GAT GTT Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val	624
195 200 205	
ATC TCA GGG CTA TTA TCG GGC GCA ACA GCT GCA CTT GTA CTT GCA GAT Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp	672
210 215 220	
AAA AAT GCT TCA ACA GCT AAA AAA GTG GGT GCG GGT TTT GAA TTG GCA Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala	720
225 230 235 240	

AAC CAA GTT GGT AAT ATT ACC AAA GCC GTT TCT TCT TAC ATT TTA Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu 245 250 255	768
GCC CAA CGT GTT GCA GCA GGT TTA TCT TCA ACT GGG CCT GTG GCT GCT Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala 260 265 270	816
TTA ATT GCT TCT ACT GTT TCT CTT GCG ATT AGC CCA TTA GCA TTT GCC Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala 275 280 285	864
GGT ATT GCC GAT AAA TTT AAT CAT GCA AAA AGT TTA GAG AGT TAT GCC Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala 290 295 300	912
GAA CGC TTT AAA AAA TTA GGC TAT GAC GGA GAT AAT TTA TTA GCA GAA Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu 305 310 315 320	960
TAT CAG CGG GGA ACA GGG ACT ATT GAT GCA TCG GTT ACT GCA ATT AAT Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn 325 330 335	1008
ACC GCA TTG GCC GCT ATT GCT GGT GTG TCT GCT GCT GCA GCC GGC Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Gly 340 345 350	1056
TCG GTT ATT GCT TCA CCG ATT GCC TTA TTA GTA TCT GGG ATT ACC GGT Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly 355 360 365	1104
GTA ATT TCT ACG ATT CTG CAA TAT TCT AAA CAA GCA ATG TTT GAG CAC Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His 370 375 380	1152
GTT GCA AAT AAA ATT CAT AAC AAA ATT GTA GAA TGG GAA AAA AAT AAT Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn 385 390 395 400	1200
CAC GGT AAG AAC TAC TTT GAA AAT GGT TAC GAT GCC CGT TAT CTT GCG His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala 405 410 415	1248
AAT TTA CAA GAT AAT ATG AAA TTC TTA CTG AAC TTA AAC AAA GAG TTA Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu 420 425 430	1296
CAG GCA GAA CGT GTC ATC GCT ATT ACT CAG CAG CAA TGG GAT AAC AAC Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Gln Trp Asp Asn Asn 435 440 445	1344
ATT GGT GAT TTA GCT GGT ATT AGC CGT TTA GGT GAA AAA GTC CTT AGT Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser 450 455 460	1392
GGT AAA GCC TAT GTG GAT GCG TTT GAA GAA GGC AAA CAC ATT AAA GCC Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala 465 470 475 480	1440

GAT AAA TTA GTA CAG TTG GAT TCG GCA AAC GGT ATT ATT GAT GTG AGT Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser 485 490 495	1488
AAT TCG GGT AAA GCG AAA ACT CAG CAT ATC TTA TTC AGA ACG CCA TTA Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu 500 505 510	1536
TTG ACG CCG GGA ACA GAG CAT CGT GAA CGC GTA CAA ACA GGT AAA TAT Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr 515 520 525	1584
GAA TAT ATT ACC AAG CTC AAT ATT AAC CGT GTA GAT AGC TGG AAA ATT Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile 530 535 540	1632
ACA GAT GGT GCA GCA AGT TCT ACC TTT GAT TTA ACT AAC GTT GTT CAG Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln 545 550 555 560	1680
CGT ATT GGT ATT GAA TTA GAC AAT GCT GGA AAT GTA ACT AAA ACC AAA Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys 565 570 575	1728
GAA ACA AAA ATT ATT GCC AAA CTT GGT GAA GGT GAT GAC AAC GTA TTT Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe 580 585 590	1776
GTT GGT TCT GGT ACG ACG GAA ATT GAT GGC GGT GAA GGT TAC GAC CGA Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Glu Gly Tyr Asp Arg 595 600 605	1824
GTT CAC TAT AGC CGT GGA AAC TAT GGT GCT TTA ACT ATT GAT GCA ACC Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr 610 615 620	1872
AAA GAG ACC GAG CAA GGT AGT TAT ACC GTA AAT CGT TTC GTA GAA ACC Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr 625 630 635 640	1920
GGT AAA GCA CTA CAC GAA GTG ACT TCA ACC CAT ACC GCA TTA GTG GGC Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly 645 650 655	1968
AAC CGT GAA GAA AAA ATA GAA TAT CGT CAT AGC AAT AAC CAG CAC CAT Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His 660 665 670	2016
GCC GGT TAT TAC ACC AAA GAT ACC TTG AAA GCT GTT GAA GAA ATT ATC Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile 675 680 685	2064
GGT ACA TCA CAT AAC GAT ATC TTT AAA GGT AGT AAG TTC AAT GAT GCC Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala 690 695 700	2112
TTT AAC GGT GGT GAT GTC GAT ACT ATT GAC GGT AAC GAC GGC AAT Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn 705 710 715 720	2160

GAC CGC TTA TTT GGT GGT AAA GGC GAT GAT ATT CTC GAT GGT GGA AAT Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn 725 730 735	2208
GGT GAT GAT TTT ATC GAT GGC GGT AAA GGC AAC GAC CTA TTA CAC GGT Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly 740 745 750	2256
GGC AAG GGC GAT GAT ATT TTC GTT CAC CGT AAA GGC GAT GGT AAT GAT Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp 755 760 765	2304
ATT ATT ACC GAT TCT GAC GGC AAT GAT AAA TTA TCA TTC TCT GAT TCG Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser 770 775 780	2352
AAC TTA AAA GAT TTA ACA TTT GAA AAA GTT AAA CAT AAT CTT GTC ATC Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile 785 790 795 800	2400
ACG AAT AGC AAA AAA GAG AAA GTG ACC ATT CAA AAC TGG TTC CGA GAG Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu 805 810 815	2448
GCT GAT TTT GCT AAA GAA GTG CCT AAT TAT AAA GCA ACT AAA GAT GAG Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu 820 825 830	2496
AAA ATC GAA GAA ATC ATC GGT CAA AAT GGC GAG CGG ATC ACC TCA AAG Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys 835 840 845	2544
CAA GTT GAT GAT CTT ATC GCA AAA GGT AAC GGC AAA ATT ACC CAA GAT Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp 850 855 860	2592
GAG CTA TCA AAA GTT GTT GAT AAC TAT GAA TTG CTC AAA CAT AGC AAA Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys 865 870 875 880	2640
AAT GTG ACA AAC AGC TTA GAT AAG TTA ATC TCA TCT GTA AGT GCA TTT Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe 885 890 895	2688
ACC TCG TCT AAT GAT TCG AGA AAT GTA TTA GTG GCT CCA ACT TCA ATG Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met 900 905 910	2736
TTG GAT CAA AGT TTA TCT CTT CAA TTT GCT AGG GGA TCC Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser 915 920 925	2778
TAGCTAGCTA GCCATG	2794

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 926 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys
1 5 10 15

Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly
20 25 30

Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu
35 40 45

Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu
50 55 60

Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu
65 70 75 80

Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln
85 90 95

Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys
100 105 110

Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly
115 120 125

Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu
130 135 140

Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala
145 150 155 160

Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe
165 170 175

Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys
180 185 190

Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val
195 200 205

Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp
210 215 220

Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala
225 230 235 240

Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu
245 250 255

Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala
260 265 270

Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala
 275 280 285
 Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala
 290 295 300
 Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu
 305 310 315 320
 Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn
 325 330 335
 Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Ala Gly
 340 345 350
 Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly
 355 360 365
 Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His
 370 375 380
 Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn
 385 390 395 400
 His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala
 405 410 415
 Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu
 420 425 430
 Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Trp Asp Asn Asn
 435 440 445
 Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser
 450 455 460
 Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala
 465 470 475 480
 Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser
 485 490 495
 Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu
 500 505 510
 Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr
 515 520 525
 Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile
 530 535 540
 Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln
 545 550 555 560
 Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys
 565 570 575
 Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe
 580 585 590
 Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg
 595 600 605

Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr
610 615 620

Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr
625 630 635 640

Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly
645 650 655

Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His
660 665 670

Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile
675 680 685

Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala
690 695 700

Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn
705 710 715 720

Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn
725 730 735

Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly
740 745 750

Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp
755 760 765

Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser
770 775 780

Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile
785 790 795 800

Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu
805 810 815

Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu
820 825 830

Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys
835 840 845

Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp
850 855 860

Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys
865 870 875 880

Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe
885 890 895

Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met
900 905 910

Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser
915 920 925

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCCAGCTC TTCTGCCGGC TGCAAAACT TCTTCTGGAA AACCTTCACC AGCTGCTAGG

60

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCCCTAGC AGCTGGTGAA GGTTTCCAG AAGAAGTTT TGCAGCCGGC AGAAGAGCTG

60

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCTCAGCA TTGGAGCTAC GGCCTGCGCC CTGGCTAAG

39

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCCTTAGC CAGGGCGCAG GCCGTAGCTC CAATGCTGA

39

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCTTGCAA CATTGTGCCT GTGAGCATTG TGAGCCGCAA CATTGTGTAC ACCCGCGCGC	60
AACCTAACCA AGACATTGTG TAG	83

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATCCTACAC AATGTCTTGG TTAAGTTGCG CGCGGGTGTACACAATGTTG CGGCTCACAA	60
TCGTCACAGG CACAATGTTG CAA	83

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2838 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..2829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GCT ACT GTT ATA GAT CTA AGC TTC CCA AAA ACT GGG GCA AAA AAA Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys	48
1 5 10 15	

ATT ATC CTC TAT ATT CCC CAA AAT TAC CAA TAT GAT ACT GAA CAA GGT Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly	96
20 25 30	

AAT GGT TTA CAG GAT TTA GTC AAA GCG GCC GAA GAG TTG GGG ATT GAG Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu	144
35 40 45	

GTA CAA AGA GAA GAA CGC AAT AAT ATT GCA ACA GCT CAA ACC AGT TTA Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu 50 55 60	192
GGC ACG ATT CAA ACC GCT ATT GGC TTA ACT GAG CGT GGC ATT GTG TTA Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu 65 70 75 80	240
TCC GCT CCA CAA ATT GAT AAA TTG CTA CAG AAA ACT AAA GCA GGC CAA Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln 85 90 95	288
GCA TTA GGT TCT GCC GAA AGC ATT GTA CAA AAT GCA AAT AAA GCC AAA Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys 100 105 110	336
ACT GTA TTA TCT GGC ATT CAA TCT ATT TTA GGC TCA GTA TTG GCT GGA Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly 115 120 125	384
ATG GAT TTA GAT GAG GCC TTA CAG AAT AAC AGC AAC CAA CAT GCT CTT Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu 130 135 140	432
GCT AAA GCT GGC TTG GAG CTA ACA AAT TCA TTA ATT GAA AAT ATT GCT Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala 145 150 155 160	480
AAT TCA GTA AAA ACA CTT GAC GAA TTT GGT GAG CAA ATT AGT CAA TTT Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe 165 170 175	528
GGT TCA AAA CTA CAA AAT ATC AAA GGC TTA GGG ACT TTA GGA GAC AAA Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys 180 185 190	576
CTC AAA AAT ATC GGT GGA CTT GAT AAA GCT GGC CTT GGT TTA GAT GTT Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val 195 200 205	624
ATC TCA GGG CTA TTA TCG GGC GCA ACA GCT GCA CTT GTA CTT GCA GAT Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp 210 215 220	672
AAA AAT GCT TCA ACA GCT AAA AAA GTG GGT GCG GGT TTT GAA TTG GCA Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala 225 230 235 240	720
AAC CAA GTT GTT GGT AAT ATT ACC AAA GCC GTT TCT TCT TAC ATT TTA Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu 245 250 255	768
GCC CAA CGT GTT GCA GCA GGT TTA TCT TCA ACT GGG CCT GTG GCT GCT Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala 260 265 270	816
TTA ATT GCT TCT ACT GTT TCT CTT GCG ATT AGC CCA TTA GCA TTT GCC Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala 275 280 285	864

GGT ATT GCC GAT AAA TTT AAT CAT GCA AAA AGT TTA GAG AGT TAT GCC Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala 290 295 300	912
GAA CGC TTT AAA AAA TTA GGC TAT GAC GGA GAT AAT TTA TTA GCA GAA Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu 305 310 315 320	960
TAT CAG CGG GGA ACA GGG ACT ATT GAT GCA TCG GTT ACT GCA ATT AAT Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn 325 330 335	1008
ACC GCA TTG GCC GCT ATT GCT GGT GTG TCT GCT GCT GCA GCC GGC Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Gly 340 345 350	1056
TCG GTT ATT GCT TCA CCG ATT GCC TTA TTA GTA TCT GGG ATT ACC GGT Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly 355 360 365	1104
GTA ATT TCT ACG ATT CTG CAA TAT TCT AAA CAA GCA ATG TTT GAG CAC Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His 370 375 380	1152
GTT GCA AAT AAA ATT CAT AAC AAA ATT GTA GAA TGG GAA AAA AAT AAT Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn 385 390 395 400	1200
CAC GGT AAG AAC TAC TTT GAA AAT GGT TAC GAT GCC CGT TAT CTT GCG His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala 405 410 415	1248
AAT TTA CAA GAT AAT ATG AAA TTC TTA CTG AAC TTA AAC AAA GAG TTA Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu 420 425 430	1296
CAG GCA GAA CGT GTC ATC GCT ATT ACT CAG CAG CAA TGG GAT AAC AAC Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Trp Asp Asn Asn 435 440 445	1344
ATT GGT GAT TTA GCT GGT ATT AGC CGT TTA GGT GAA AAA GTC CTT AGT Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser 450 455 460	1392
GGT AAA GCC TAT GTG GAT GCG TTT GAA GAA GGC AAA CAC ATT AAA GCC Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala 465 470 475 480	1440
GAT AAA TTA GTA CAG TTG GAT TCG GCA AAC GGT ATT ATT GAT GTG AGT Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser 485 490 495	1488
AAT TCG GGT AAA GCG AAA ACT CAG CAT ATC TTA TTC AGA ACG CCA TTA Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu 500 505 510	1536
TTG ACG CCG GGA ACA GAG CAT CGT GAA CGC GTA CAA ACA GGT AAA TAT Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr 515 520 525	1584

GAA TAT ATT ACC AAG CTC AAT AAC CGT GTA GAT AGC TGG AAA ATT Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile 530 535 540	1632
ACA GAT GGT GCA GCA AGT TCT ACC TTT GAT TTA ACT AAC GTT GTT CAG Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln 545 550 555 560	1680
CGT ATT GGT ATT GAA TTA GAC AAT GCT GGA AAT GTA ACT AAA ACC AAA Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys 565 570 575	1728
GAA ACA AAA ATT ATT GCC AAA CTT GGT GAA GGT GAT GAC AAC GTA TTT Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe 580 585 590	1776
GTT GGT TCT GGT ACG ACG GAA ATT GAT GGC GGT GAA GGT TAC GAC CGA Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Tyr Asp Arg 595 600 605	1824
GTT CAC TAT AGC CGT GGA AAC TAT GGT GCT TTA ACT ATT GAT GCA ACC Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr 610 615 620	1872
AAA GAG ACC GAG CAA GGT AGT TAT ACC GTA AAT CGT TTC GTA GAA ACC Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr 625 630 635 640	1920
GGT AAA GCA CTA CAC GAA GTG ACT TCA ACC CAT ACC GCA TTA GTG GGC Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly 645 650 655	1968
AAC CGT GAA GAA AAA ATA GAA TAT CGT CAT AGC AAT AAC CAG CAC CAT Asn Arg Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His 660 665 670	2016
GCC GGT TAT TAC ACC AAA GAT ACC TTG AAA GCT GTT GAA GAA ATT ATC Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile 675 680 685	2064
GGT ACA TCA CAT AAC GAT ATC TTT AAA GGT AGT AAG TTC AAT GAT GCC Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala 690 695 700	2112
TTT AAC GGT GGT GAT GTC GAT ACT ATT GAC GGT AAC GAC GGC AAT Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn 705 710 715 720	2160
GAC CGC TTA TTT GGT GGT AAA GGC GAT GAT ATT CTC GAT GGT GGA AAT Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn 725 730 735	2208
GGT GAT GAT TTT ATC GAT GGC GGT AAA GGC AAC GAC CTA TTA CAC GGT Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly 740 745 750	2256
GGC AAG GGC GAT GAT ATT TTC GTT CAC CGT AAA GGC GAT GGT AAT GAT Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp 755 760 765	2304

ATT ATT ACC GAT TCT GAC GGC AAT GAT AAA TTA TCA TTC TCT GAT TCG Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser 770 775 780	2352
AAC TTA AAA GAT TTA ACA TTT GAA AAA GTT AAA CAT AAT CTT GTC ATC Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile 785 790 795 800	2400
ACG AAT AGC AAA AAA GAG AAA GTG ACC ATT CAA AAC TGG TTC CGA GAG Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu 805 810 815	2448
GCT GAT TTT GCT AAA GAA GTG CCT AAT TAT AAA GCA ACT AAA GAT GAG Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu 820 825 830	2496
AAA ATC GAA GAA ATC ATC GGT CAA AAT GGC GAG CGG ATC ACC TCA AAG Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys 835 840 845	2544
CAA GTT GAT GAT CTT ATC GCA AAA GGT AAC GGC AAA ATT ACC CAA GAT Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Ile Thr Gln Asp 850 855 860	2592
GAG CTA TCA AAA GTT GTT GAT AAC TAT GAA TTG CTC AAA CAT AGC AAA Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys 865 870 875 880	2640
AAT GTG ACA AAC AGC TTA GAT AAG TTA ATC TCA TCT GTA AGT GCA TTT Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe 885 890 895	2688
ACC TCG TCT AAT GAT TCG AGA AAT GTA TTA GTG GCT CCA ACT TCA ATG Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met 900 905 910	2736
TTG GAT CAA AGT TTA TCT TCT CTT CAA TTT GCT AGG GGA TCC AGC TCT Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser Ser Ser 915 920 925	2784
TCT GCC GGC TGC AAA AAC TTC TTC TGG AAA ACC TTC ACC AGC TGC Ser Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys 930 935 940	2829
TAGGGATCC	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 943 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys 1 5 10 15
Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly 20 25 30

Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu
 35 40 45

Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu
 50 55 60

Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu
 65 70 75 80

Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln
 85 90 95

Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys
 100 105 110

Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly
 115 120 125

Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu
 130 135 140

Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala
 145 150 155 160

Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe
 165 170 175

Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys
 180 185 190

Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val
 195 200 205

Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp
 210 215 220

Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala
 225 230 235 240

Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu
 245 250 255

Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala
 260 265 270

Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala
 275 280 285

Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala
 290 295 300

Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu
 305 310 315 320

Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn
 325 330 335

Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Gly
 340 345 350

Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly
 355 360 365

Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His
 370 375 380
 Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn
 385 390 395 400
 His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala
 405 410 415
 Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu
 420 425 430
 Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Trp Asp Asn Asn
 435 440 445
 Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser
 450 455 460
 Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala
 465 470 475 480
 Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser
 485 490 495
 Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu
 500 505 510
 Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr
 515 520 525
 Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile
 530 535 540
 Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln
 545 550 555 560
 Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys
 565 570 575
 Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe
 580 585 590
 Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg
 595 600 605
 Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr
 610 615 620
 Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr
 625 630 635 640
 Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly
 645 650 655
 Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His
 660 665 670
 Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile
 675 680 685
 Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala
 690 695 700

Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn
 705 710 715 720
 Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn
 725 730 735
 Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly
 740 745 750
 Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp
 755 760 765
 Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser
 770 775 780
 Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile
 785 790 795 800
 Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu
 805 810 815
 Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu
 820 825 830
 Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys
 835 840 845
 Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Ile Thr Gln Asp
 850 855 860
 Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys
 865 870 875 880
 Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe
 885 890 895
 Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met
 900 905 910
 Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser Ser Ser
 915 920 925
 Ser Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys
 930 935 940

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2817 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..2808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG GCT ACT GTT ATA GAT CTA AGC TTC CCA AAA ACT GGG GCA AAA AAA Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys	48
1 5 10 15	
ATT ATC CTC TAT ATT CCC CAA AAT TAC CAA TAT GAT ACT GAA CAA GGT Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly	96
20 25 30	
AAT GGT TTA CAG GAT TTA GTC AAA GCG GCC GAA GAG TTG GGG ATT GAG Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu	144
35 40 45	
GTA CAA AGA GAA GAA CGC AAT AAT ATT GCA ACA GCT CAA ACC AGT TTA Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu	192
50 55 60	
GGC ACG ATT CAA ACC GCT ATT GGC TTA ACT GAG CGT GGC ATT GTG TTA Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu	240
65 70 75 80	
TCC GCT CCA CAA ATT GAT AAA TTG CTA CAG AAA ACT AAA GCA GGC CAA Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln	288
85 90 95	
GCA TTA GGT TCT GCC GAA AGC ATT GTC CAA AAT GCA AAT AAA GCC AAA Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys	336
100 105 110	
ACT GTA TTA TCT GGC ATT CAA TCT ATT TTA GGC TCA GTA TTG GCT GGA Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly	384
115 120 125	
ATG GAT TTA GAT GAG GCC TTA CAG AAT AAC AGC AAC CAA CAT GCT CTT Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu	432
130 135 140	
GCT AAA GCT GGC TTG GAG CTA ACA AAT TCA TTA ATT GAA AAT ATT GCT Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala	480
145 150 155 160	
AAT TCA GTA AAA ACA CTT GAC GAA TTT GGT GAG CAA ATT AGT CAA TTT Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe	528
165 170 175	
GGT TCA AAA CTA CAA AAT ATC AAA GGC TTA GGG ACT TTA GGA GAC AAA Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys	576
180 185 190	
CTC AAA AAT ATC GGT GGA CTT GAT AAA GCT GGC CTT GGT TTA GAT GTT Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val	624
195 200 205	
ATC TCA GGG CTA TTA TCG GGC GCA ACA GCT GCA CTT GTA CTT GCA GAT Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp	672
210 215 220	
AAA AAT GCT TCA ACA GCT AAA AAA GTG GGT GCG GGT TTT GAA TTG GCA Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala	720
225 230 235 240	

AAC CAA GTT GTT GGT AAT ATT ACC AAA GCC GTT TCT TCT TAC ATT TTA Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu 245 250 255	768
GCC CAA CGT GTT GCA GCA GGT TTA TCT TCA ACT GGG CCT GTG GCT GCT Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala 260 265 270	816
TTA ATT GCT TCT ACT GTT CTT GCG ATT AGC CCA TTA GCA TTT GCC Leu Ile Ala Ser Thr Val Ala Ile Ser Pro Leu Ala Phe Ala 275 280 285	864
GGT ATT GCC GAT AAA TTT AAT CAT GCA AAA AGT TTA GAG AGT TAT GCC Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala 290 295 300	912
GAA CGC TTT AAA AAA TTA GGC TAT GAC GGA GAT AAT TTA TTA GCA GAA Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu 305 310 315 320	960
TAT CAG CGG GGA ACA GGG ACT ATT GAT GCA TCG GTT ACT GCA ATT AAT Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn 325 330 335	1008
ACC GCA TTG GCC GCT ATT GCT GGT GTG TCT GCT GCT GCA GCC GGC Thr Ala Leu Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Ala Gly 340 345 350	1056
TCG GTT ATT GCT TCA CCG ATT GCC TTA TTA GTA TCT GGG ATT ACC GGT Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly 355 360 365	1104
GTA ATT TCT ACG ATT CTG CAA TAT TCT AAA CAA GCA ATG TTT GAG CAC Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His 370 375 380	1152
GTT GCA AAT AAA ATT CAT AAC AAA ATT GTA GAA TGG GAA AAA AAT AAT Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn 385 390 395 400	1200
CAC GGT AAG AAC TAC TTT GAA AAT GGT TAC GAT GCC CGT TAT CTT GCG His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala 405 410 415	1248
AAT TTA CAA GAT AAT ATG AAA TTC TTA CTG AAC TTA AAC AAA GAG TTA Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu 420 425 430	1296
CAG GCA GAA CGT GTC ATC GCT ATT ACT CAG CAG CAA TGG GAT AAC AAC Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Gln Trp Asp Asn Asn 435 440 445	1344
ATT GGT GAT TTA GCT GGT ATT AGC CGT TTA GGT GAA AAA GTC CTT AGT Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser 450 455 460	1392
GGT AAA GCC TAT GTG GAT GCG TTT GAA GAA GGC AAA CAC ATT AAA GCC Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala 465 470 475 480	1440

GAT AAA TTA GTA CAG TTG GAT TCG GCA AAC GGT ATT ATT GAT GTG AGT Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser 485	490	495	1488	
AAT TCG GGT AAA GCG AAA ACT CAG CAT ATC TTA TTC AGA ACG CCA TTA Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu 500	505	510	1536	
TTG ACG CCG GGA ACA GAG CAT CGT GAA CGC GTA CAA ACA GGT AAA TAT Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr 515	520	525	1584	
GAA TAT ATT ACC AAG CTC AAT ATT AAC CGT GTA GAT AGC TGG AAA ATT Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile 530	535	540	1632	
ACA GAT GGT GCA GCA AGT TCT ACC TTT GAT TTA ACT AAC GTT GTT CAG Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln 545	550	555	560	1680
CGT ATT GGT ATT GAA TTA GAC AAT GCT GGA AAT GTA ACT AAA ACC AAA Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys 565	570	575	1728	
GAA ACA AAA ATT ATT GCC AAA CTT GGT GAA GGT GAT GAC AAC GTA TTT Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe 580	585	590	1776	
GTT GGT TCT GGT ACG ACG GAA ATT GAT GGC GGT GAA GGT TAC GAC CGA Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg 595	600	605	1824	
GTT CAC TAT AGC CGT GGA AAC TAT GGT GCT TTA ACT ATT GAT GCA ACC Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr 610	615	620	1872	
AAA GAG ACC GAG CAA GGT AGT TAT ACC GTA AAT CGT TTC GTA GAA ACC Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr 625	630	635	640	1920
GGT AAA GCA CTA CAC GAA GTG ACT TCA ACC CAT ACC GCA TTA GTG GGC Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly 645	650	655	1968	
AAC CGT GAA GAA AAA ATA GAA TAT CGT CAT AGC AAT AAC CAG CAC CAT Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His 660	665	670	2016	
GCC GGT TAT TAC ACC AAA GAT ACC TTG AAA GCT GTT GAA GAA ATT ATC Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile 675	680	685	2064	
GGT ACA TCA CAT AAC GAT ATC TTT AAA GGT AGT AAG TTC AAT GAT GCC Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala 690	695	700	2112	
TTT AAC GGT GGT GAT GTC GAT ACT ATT GAC GGT AAC GAC GGC AAT Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn 705	710	715	720	2160

GAC CGC TTA TTT GGT GGT AAA GGC GAT GAT ATT CTC GAT GGT GGA AAT Asp Arg Leu Phe Gly Gly Lys Asp Asp Ile Leu Asp Gly Gly Asn 725 730 735	2208
GGT GAT GAT TTT ATC GAT GGC GGT AAA GGC AAC GAC CTA TTA CAC GGT Gly Asp Asp Phe Ile Asp Gly Gly Lys Asn Asp Leu Leu His Gly 740 745 750	2256
GGC AAG GGC GAT GAT ATT TTC GTT CAC CGT AAA GGC GAT GGT AAT GAT Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp 755 760 765	2304
ATT ATT ACC GAT TCT GAC GGC AAT GAT AAA TTA TCA TTC TCT GAT TCG Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser 770 775 780	2352
AAC TTA AAA GAT TTA ACA TTT GAA AAA GTT AAA CAT AAT CTT GTC ATC Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile 785 790 795 800	2400
ACG AAT AGC AAA AAA GAG AAA GTG ACC ATT CAA AAC TGG TTC CGA GAG Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu 805 810 815	2448
GCT GAT TTT GCT AAA GAA GTG CCT AAT TAT AAA GCA ACT AAA GAT GAG Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu 820 825 830	2496
AAA ATC GAA GAA ATC ATC GGT CAA AAT GGC GAG CGG ATC ACC TCA AAG Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys 835 840 845	2544
CAA GTT GAT GAT CTT ATC GCA AAA GGT AAC GGC AAA ATT ACC CAA GAT Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp 850 855 860	2592
GAG CTA TCA AAA GTT GTT GAT AAC TAT GAA TTG CTC AAA CAT AGC AAA Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys 865 870 875 880	2640
AAT GTG ACA AAC AGC TTA GAT AAG TTA ATC TCA TCT GTA AGT GCA TTT Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe 885 890 895	2688
ACC TCG TCT AAT GAT TCG AGA AAT GTA TTA GTG GCT CCA ACT TCA ATG Thr Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met 900 905 910	2736
TTG GAT CAA AGT TTA TCT CTT CAA TTT GCT AGG GGA TCT CAG CAT Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser Gln His 915 920 925	2784
TGG AGC TAC GGC CTG CGC CCT GGC TAAGGATCC Trp Ser Tyr Gly Leu Arg Pro Gly 930 935	2817

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 936 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys
1 5 10 15

Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly
20 25 30

Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu
35 40 45

Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu
50 55 60

Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu
65 70 75 80

Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln
85 90 95

Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys
100 105 110

Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly
115 120 125

Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu
130 135 140

Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala
145 150 155 160

Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe
165 170 175

Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys
180 185 190

Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val
195 200 205

Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp
210 215 220

Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala
225 230 235 240

Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu
245 250 255

Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala
260 265 270

Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala
 275 280 285
 Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala
 290 295 300
 Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu
 305 310 315 320
 Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn
 325 330 335
 Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Gly
 340 345 350
 Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly
 355 360 365
 Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His
 370 375 380
 Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn
 385 390 395 400
 His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala
 405 410 415
 Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu
 420 425 430
 Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Trp Asp Asn Asn
 435 440 445
 Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser
 450 455 460
 Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala
 465 470 475 480
 Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser
 485 490 495
 Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu
 500 505 510
 Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr
 515 520 525
 Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile
 530 535 540
 Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln
 545 550 555 560
 Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys
 565 570 575
 Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe
 580 585 590
 Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg
 595 600 605

Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr
 610 615 620
 Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr
 625 630 635 640
 Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly
 645 650 655
 Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His
 660 665 670
 Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile
 675 680 685
 Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala
 690 695 700
 Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn
 705 710 715 720
 Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn
 725 730 735
 Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly
 740 745 750
 Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp
 755 760 765
 Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser
 770 775 780
 Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile
 785 790 795 800
 Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu
 805 810 815
 Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu
 820 825 830
 Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys
 835 840 845
 Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp
 850 855 860
 Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys
 865 870 875 880
 Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe
 885 890 895
 Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met
 900 905 910
 Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser Gln His
 915 920 925
 Trp Ser Tyr Gly Leu Arg Pro Gly
 930 935

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2861 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG GCT ACT GTT ATA GAT CTA AGC TTC CCA AAA ACT GGG GCA AAA AAA	48
Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys	
1 5 10 15	
ATT ATC CTC TAT ATT CCC CAA AAT TAC CAA TAT GAT ACT GAA CAA GGT	96
Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly	
20 25 30	
AAT GGT TTA CAG GAT TTA GTC AAA GCG GCC GAA GAG TTG GGG ATT GAG	144
Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu	
35 40 45	
GTA CAA AGA GAA CGC AAT AAT ATT GCA ACA GCT CAA ACC AGT TTA	192
Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu	
50 55 60	
GGC ACG ATT CAA ACC GCT ATT GGC TTA ACT GAG CGT GGC ATT GTG TTA	240
Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu	
65 70 75 80	
TCC GCT CCA CAA ATT GAT AAA TTG CTA CAG AAA ACT AAA GCA GGC CAA	288
Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln	
85 90 95	
GCA TTA GGT TCT GCC GAA AGC ATT GTA CAA AAT GCA AAT AAA GCC AAA	336
Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys	
100 105 110	
ACT GTA TTA TCT GGC ATT CAA TCT ATT TTA GGC TCA GTA TTG GCT GGA	384
Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly	
115 120 125	
ATG GAT TTA GAT GAG GCC TTA CAG AAT AAC AGC AAC CAA CAT GCT CTT	432
Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu	
130 135 140	
GCT AAA GCT GGC TTG GAG CTA ACA AAT TCA TTA ATT GAA AAT ATT GCT	480
Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala	
145 150 155 160	
AAT TCA GTA AAA ACA CTT GAC GAA TTT GGT GAG CAA ATT AGT CAA TTT	528
Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe	
165 170 175	

GGT TCA AAA CTA CAA AAT ATC AAA GGC TTA GGG ACT TTA GGA GAC AAA Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys 180 185 190	576
CTC AAA AAT ATC GGT GGA CTT GAT AAA GCT GGC CTT GGT TTA GAT GTT Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val 195 200 205	624
ATC TCA GGG CTA TTA TCG GGC GCA ACA GCT GCA CTT GTA CTT GCA GAT Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp 210 215 220	672
AAA AAT GCT TCA ACA GCT AAA AAA GTG GGT GCG GGT TTT GAA TTG GCA Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala 225 230 235 240	720
AAC CAA GTT GTT GGT AAT ATT ACC AAA GCC GTT TCT TCT TAC ATT TTA Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu 245 250 255	768
GCC CAA CGT GTT GCA GCA GGT TTA TCT TCA ACT GGG CCT GTG GCT GCT Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala 260 265 270	816
TTA ATT GCT TCT ACT GTT TCT CTT GCG ATT AGC CCA TTA GCA TTT GCC Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala 275 280 285	864
GGT ATT GCC GAT AAA TTT AAT CAT GCA AAA AGT TTA GAG AGT TAT GCC Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala 290 295 300	912
GAA CGC TTT AAA AAA TTA GGC TAT GAC GGA GAT AAT TTA TTA GCA GAA Glu Arg Phe Lys, Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu 305 310 315 320	960
TAT CAG CGG GGA ACA GGG ACT ATT GAT GCA TCG GTT ACT GCA ATT AAT Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn 325 330 335	1008
ACC GCA TTG GCC GCT ATT GCT GGT GTG TCT GCT GCT GCA GCC GGC Thr Ala Leu Ala Ala Ile Ala Gly Val Ser Ala Ala Ala Gly 340 345 350	1056
TCG GTT ATT GCT TCA CCG ATT GCC TTA TTA GTA TCT GGG ATT ACC GGT Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly 355 360 365	1104
GTA ATT TCT ACG ATT CTG CAA TAT TCT AAA CAA GCA ATG TTT GAG CAC Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His 370 375 380	1152
GTT GCA AAT AAA ATT CAT AAC AAA ATT GTA GAA TGG GAA AAA AAT AAT Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn 385 390 395 400	1200
CAC GGT AAG AAC TAC TTT GAA AAT GGT TAC GAT GCC CGT TAT CTT GCG His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala 405 410 415	1248

AAT TTA CAA GAT AAT ATG AAA TTC TTA CTG AAC TTA AAC AAA GAG TTA Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu 420 425 430	1296
CAG GCA GAA CGT GTC ATC GCT ATT ACT CAG CAG CAA TGG GAT AAC AAC Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Trp Asp Asn Asn 435 440 445	1344
ATT GGT GAT TTA GCT GGT ATT AGC CGT TTA GGT GAA AAA GTC CTT AGT Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser 450 455 460	1392
GGT AAA GCC TAT GTG GAT GCG TTT GAA GAA GGC AAA CAC ATT AAA GCC Gly Lys Ala Tyr Val Asp Ala Phe Glu Gly Lys His Ile Lys Ala 465 470 475 480	1440
GAT AAA TTA GTA CAG TTG GAT TCG GCA AAC GGT ATT ATT GAT GTG AGT Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser 485 490 495	1488
AAT TCG GGT AAA GCG AAA ACT CAG CAT ATC TTA TTC AGA ACG CCA TTA Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu 500 505 510	1536
TTG ACG CCG GGA ACA GAG CAT CGT GAA CGC GTA CAA ACA GGT AAA TAT Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr 515 520 525	1584
GAA TAT ATT ACC AAG CTC AAT ATT AAC CGT GTA GAT AGC TGG AAA ATT Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile 530 535 540	1632
ACA GAT GGT GCA GCA AGT TCT ACC TTT GAT TTA ACT AAC GTT GTT CAG Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln 545 550 555 560	1680
CGT ATT GGT ATT GAA TTA GAC AAT GCT GGA AAT GTA ACT AAA ACC AAA Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys 565 570 575	1728
GAA ACA AAA ATT ATT GCC AAA CTT GGT GAA GGT GAT GAC AAC GTA TTT Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asn Val Phe 580 585 590	1776
GTT GGT TCT GGT ACG ACG GAA ATT GAT GGC GGT GAA GGT TAC GAC CGA Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Glu Gly Tyr Asp Arg 595 600 605	1824
GTT CAC TAT AGC CGT GGA AAC TAT GGT GCT TTA ACT ATT GAT GCA ACC Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr 610 615 620	1872
AAA GAG ACC GAG CAA GGT AGT TAT ACC GTA AAT CGT TTC GTA GAA ACC Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr 625 630 635 640	1920
GGT AAA GCA CTA CAC GAA GTG ACT TCA ACC CAT ACC GCA TTA GTG GGC Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly 645 650 655	1968

AAC CGT GAA GAA AAA ATA GAA TAT CGT CAT AGC AAT AAC CAG CAC CAT Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His 660 665 670	2016
GCC GGT TAT TAC ACC AAA GAT ACC TTG AAA GCT GTT GAA GAA ATT ATC Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile 675 680 685	2064
GGT ACA TCA CAT AAC GAT ATC TTT AAA GGT AGT AAG TTC AAT GAT GCC Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala 690 695 700	2112
TTT AAC GGT GGT GAT GTC GAT ACT ATT GAC GGT AAC GAC GGC AAT Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn 705 710 715 720	2160
GAC CGC TTA TTT GGT GGT AAA GGC GAT GAT ATT CTC GAT GGT GGA AAT Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn 725 730 735	2208
GGT GAT GAT TTT ATC GAT GGC GGT AAA GGC AAC GAC CTA TTA CAC GGT Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly 740 745 750	2256
GGC AAG GGC GAT GAT ATT TTC GTT CAC CGT AAA GGC GAT GGT AAT GAT Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp 755 760 765	2304
ATT ATT ACC GAT TCT GAC GGC AAT GAT AAA TTA TCA TTC TCT GAT TCG Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser 770 775 780	2352
AAC TTA AAA GAT TTA ACA TTT GAA AAA GTT AAA CAT AAT CTT GTC ATC Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile 785 790 795 800	2400
ACG AAT AGC AAA AAA GAG AAA GTG ACC ATT CAA AAC TGG TTC CGA GAG Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu 805 810 815	2448
GCT GAT TTT GCT AAA GAA GTG CCT AAT TAT AAA GCA ACT AAA GAT GAG Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu 820 825 830	2496
AAA ATC GAA GAA ATC ATC GGT CAA AAT GGC GAG CGG ATC ACC TCA AAG Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys 835 840 845	2544
CAA GTT GAT GAT CTT ATC GCA AAA GGT AAC GGC AAA ATT ACC CAA GAT Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp 850 855 860	2592
GAG CTA TCA AAA GTT GTT GAT AAC TAT GAA TTG CTC AAA CAT AGC AAA Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys 865 870 875 880	2640
AAT GTG ACA AAC AGC TTA GAT AAG TTA ATC TCA TCT GTA AGT GCA TTT Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe 885 890 895	2688

ACC TCG TCT AAT GAT TCG AGA AAT GTA TTA GTG GCT CCA ACT TCA ATG Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met 900 905 910	2736
TTG GAT CAA AGT TTA TCT TCT CAA TTT GCT AGG GGA TCT TGC AAC Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser Cys Asn 915 920 925	2784
ATT GTG CCT GTG AGC ATT GTG AGC CGC AAC ATT GTG TAC ACC CGC GCG Ile Val Pro Val Ser Ile Val Ser Arg Asn Ile Val Tyr Thr Arg Ala 930 935 940	2832
CAA CCT AAC CAA GAC ATT GTG TAGGATCC Gln Pro Asn Gln Asp Ile Val 945 950	2861

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 951 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys 1 5 10 15
Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly 20 25 30
Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu 35 40 45
Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu 50 55 60
Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu 65 70 75 80
Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln 85 90 95
Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys 100 105 110
Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly 115 120 125
Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu 130 135 140
Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala 145 150 155 160
Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe 165 170 175
Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys 180 185 190

Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val
 195 200 205
 Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp
 210 215 220
 Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala
 225 230 235 240
 Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu
 245 250 255
 Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala
 260 265 270
 Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala
 275 280 285
 Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala
 290 295 300
 Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asn Leu Leu Ala Glu
 305 310 315 320
 Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn
 325 330 335
 Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Gly
 340 345 350
 Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly
 355 360 365
 Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His
 370 375 380
 Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn
 385 390 395 400
 His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala
 405 410 415
 Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu
 420 425 430
 Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Gln Trp Asp Asn Asn
 435 440 445
 Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser
 450 455 460
 Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala
 465 470 475 480
 Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser
 485 490 495
 Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu
 500 505 510
 Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr
 515 520 525

Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile
 530 535 540
 Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln
 545 550 555 560
 Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys
 565 570 575
 Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe
 580 585 590
 Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Tyr Asp Arg
 595 600 605
 Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr
 610 615 620
 Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr
 625 630 635 640
 Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly
 645 650 655
 Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His
 660 665 670
 Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile
 675 680 685
 Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala
 690 695 700
 Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn
 705 710 715 720
 Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn
 725 730 735
 Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly
 740 745 750
 Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp
 755 760 765
 Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser
 770 775 780
 Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile
 785 790 795 800
 Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu
 805 810 815
 Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu
 820 825 830
 Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys
 835 840 845
 Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp
 850 855 860

Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys
865 870 875 880
Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe
885 890 895
Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met
900 905 910
Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser Cys Asn
915 920 925
Ile Val Pro Val Ser Ile Val Ser Arg Asn Ile Val Tyr Thr Arg Ala
930 935 940
Gln Pro Asn Gln Asp Ile Val
945 950

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "The amino acid at this location can be either Lys, Asp, Val or Asn."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "The amino acid at this location can be either Lys, Asp, Val or Asn."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Gly Xaa Gly Xaa Asp
1 5